

JC668 U.S. PRO
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(5') 1 SDLEQERRAKEKLQEQQ
18 SDLEQDRLAKEKLQEQQ
35 SDLEQERLAKEKLQEQQ
52 SDLEQERRAKEKLQEQQ
69 SDLEQERRAKEKLQEQQ
86 SDLEQDRLAKEKLQEQQ
103 SDLEQERRAKEKLQEQQ
120 SDLEQERKAKEKLQEQQ
137 SDLEQERLAKEKLQEQQ
154 SDLEQERRAKEKLQEQQ
171 SDLEQERRAKEKLQEQQ
188 SDLEQERRAKEKLQEQQ
205 RDLEQ

210 RKADTKKNLERKKEHGDLAEDLYGRLEIP
240 AIELPSENERYYYIPHQSSLQPQDNRGNSRD
270 SKEISIIIEKTNRESITTNVEGRRDIHKGHL
300 EEKKDGSIKPEQKEDKS 316 (3')

FIGURE 1

(5') 1 AAAGCGATCTAGAACAGAGACCGTGCCTAAAGAAAGTTGCAAGAACAAAC
52 AAAGCGATTAGAACAGATAGACTTGCCTAAAGAAAGTTACAAGAGCAGC
103 AAAGCGATTAGAACAGAGACCTTGCTAAAGAAAGTTGCAAGAACAAAC
154 AAAGCGATCTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
205 AAAGCGATTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
256 AAAGCGATTAGAACAGAACAGAACAGAGACGTTGCTAAAGAAAGTTACAAGAGCAGC
307 AAAGCGATTAGAACAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
358 AAAGCGATTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
409 AAAGCGATTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
460 AAAGCGATTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
511 AAAGCGATTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAACAAAC
562 AAAGCGATTAGAACAGAACAGAGACGTTGCTAAAGAAAGTTGCAAGAGCAGC
613 AAAGGATTAGAACAA
630 AGGAAGGCTGATACGAAAAAAATTAGAAAGAAAAAGGAAACATGGAGAT
681 ATATTAGCAGGATTATATGGCGTTAGAAATACCAGCTATAGAACTT
732 CCATCAGAAAATGAACTGGATATTATACCCACATCAATCTTACCT
783 CAGGACAACAGAGGGAAATAGTAGGATTCCAGGAATATCTATAATAGAA
834 AAAACAAATAGAGAATCTTACACAAATGTTGAAGGACCAAGGGATATA
885 CATAAAGGACATCTTGAAAGAAAGATGGTCAATAAAACCAGAACAA
936 AAAGAAGATAATCT 950 (3')

FIGURE 2

RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVKSVQQEQQ
HNVEEKVEESVEENDEESVEENVEENVEENDGSVASSVEESI
ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE
ESVAPSVEESVAEMLKER

FIGURE 3

5' GAA TTC CGT GAT GAA CTT TTT AAT GAA TTA TTA AAT AGT GTA GAT
GTT AAT GGA GAA GTA AAA GAA AAT ATT TGA GAG GAA AGT CAA GTT AAT
GAG GAT ATT TTT AAT AGT TTA GTA AAA AGT GTT CAA CAA GAA CAA CAA
CAC AAT GTT GAA GAA AA AGT TGA AGA AAG TGT AGA AGA AA ATG ACG
AAG AAA GTG TAG AAG AAA ATG TAG AAG AAA ATG TAG AAG AAA ATG
ACG ACG GAA GTG TAG CCT CAA GTG TTG AAG AAA GTA TAG CTT CAA GTG
TTG ATG AAA GTA TAG ATT CAA GTA TTG AAG AAA ATG TAG CTC CAA CTG
TTG AAG AAA TCG TAG CTC CAA CTG TTG AAG AAA TTG TAG CTC CAA GTG
TTG TAG AAA AGT GTG CTC CAA GTG TTG AAG AAA GTG TAG CTC CAA GTG
TTG AAG AAA GTG TAG CTG AAA TGT TGA AGG AAA GGA ATT C 3'

FIGURE 4

NSRDSKEISIIEKTNRESITTNVEGRRDIHK

LSA-TER

729S-NRI
729S-NRII
729S-Rep

DELFNELLNSVVDVNGEVKENILEESQ
LEESQVNDDIFSNSLVKSVQQEQQHNV
VEKCAPSVEEVAPSVEESVAEMLKER

FIGURE 5

NUCLEOTIDE SEQUENCE OF THE LSA GENE
5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTACTTCTTAAA

(CODING 5' END, UNIQUE)

33 ATGAAACATATTTGTACATATCATTACTTATCCTGTTAATTATTG
84 ATATTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA
135 TAAAATCTAACCTGAGAAGTGGTTCTCAAATTCTAGGAATCGAATAATGA
186 GGAAAATCACGAGAAGAACACGTTTATCTCATAATTATGAGAAAAACT
237 AAAAATAATGAAAATAATAAATTTCGATAAGGATAAAGAGTTAACGATGT
288 CTAATGTAAGGAAATGTGTCACAAACAAATTCAAAAGTCTTTAAGAAATCT
339 TGGTGTTCAGAGAATATTCCTTAAAGAAAATAATTAAATAAGGAAGGG
390 AAATTAAATTGAACACATAATAAATGATGATGACGATAAAAAAAATATTA
441 AAGGGCAAGACGAAAACAGACAAGAAGATCTGAAGAAAAAGCA

(CODING 5' END, repetitive)

492 GCTAAAGAAAAGTTACAGGGCAACAAAGCGATTCAGAACAAGAGAGACGT
543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACCT
594 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
645 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACCT
696 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
747 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
798 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACCT
849 GCTAAAGAAAAGTTACAAGAGAGCAGAAAGCGATTTAGAACAAGAATAGACCT
900 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
951 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGA 988

FIGURE 6

LSA. 5' /ATG - -> 1-phase Translation

DNA sequence 956 b.p. ATGAAACATATT ... AAGCGATTAGA linear

1 / 1 31 / 11
ATG AAA CAT ATT TTG TAC ATA TCA TTT TAC ATC CTT GTT AAT TTA TTG ATA TTT CAT
met lys his ile leu tyr ile ser phe tyr phe ile leu val asn leu ile phe his
61 / 21 91 / 31
ATA AAT GGA AAG ATA ATA AAG AAT TCT GAA AAA GAT GAA ATC ATA AAA TCT AAC TTG AGA
ile asn gly lys ile ile lys asn ser glu lys asp glu ile ile lys ser asn leu arg
121 / 41 151 / 51
AGT GGT TCT TCA AAT TCT AGG AAT CGA ATA AAT GAG GAA AAT CAC GAG AAG AAA CAC GTT
ser gly ser ser asn ser arg ile asn arg ile asn glu glu asn his glu lys lys his val
181 / 61 211 / 71
TTA TCT CAT AAT TCA TAT GAG AAA ACT AAA AAT AAT GAA AAT AAA TTT TTC GAT AAG
leu ser his asn ser tyr glu lys thr lys asn asn glu asn asn lys phe phe asp lys
241 / 81 271 / 91
GAT AAA GAG TTA ACG ATG TCT AAT GTA AAA AAT GTG TCA CAA ACA AAT TTC AAA AGT CTT
asp lys glu leu thr met ser asn val lys asn val ser gln thr asn phe lys ser leu
301 / 101 331 / 111
TTA AGA AAT CTT GGT TCA GAG AAT ATA TTC CTT AAA GAA AAT AAA TTA AAT AAG GAA
leu arg asn leu gly val ser glu asn ile phe leu lys glu asn lys leu asn lys glu

FIGURE 7A

361 / 121
GGG AAA TTA ATT GAA CAC ATA AAT GAT GAC GAT AAA AAA TAT ATT AAA GGG
gly lys leu ile glu his ile ile asn asp asp asp asp lys lys lys tyr ile lys gly
421 / 141 451 / 151
CAA GAC GAA AAC AGA CAA GAA GAT CTT GAA AAA GCA GCT AAA GAA AAG TTA CAG GGG
gln asp glu asn arg gln glu asp leu glu lys ala ala lys glu lys leu gln gly
481 / 161 511 / 171
CAA CAA AGC GAT TCA GAA CAA GAG AGA CGT AAA GAA AAG TTG CAA GAA CAA CAA AGC
gln gln ser asp ser glu gln glu arg arg ala lys glu lys leu gln glu gln ser
541 / 181 571 / 191
GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA
asp leu glu gln glu arg leu ala lys glu lys leu gln glu gln ser asp leu glu
601 / 201 631 / 211
CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAG AGA
gln glu arg arg ala lys glu lys leu gln glu gln ser asp leu glu gln glu arg
661 / 221 691 / 231
CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA
leu ala lys glu lys leu gln glu gln ser asp leu glu gln glu arg arg ala lys
721 / 241 751 / 251
GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG
glu lys leu gln glu gln ser asp leu glu gln glu arg arg ala lys glu lys leu

FIGURE 7B

781 / 261 811 / 271
CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG
gln glu gln gln ser asp leu glu gln glu gln glu gln gln gln gln gln gln gln
841 / 281 871 / 291
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT
gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp
901 / 301 931 / 311
TTA GAA CAA GAG AGA CGT GCT AAA GAA AGG TTG CAA GAA CAA CAA AGC GAT TTA
leu glu gln glu arg arg ala lys glu arg leu gln glu gln ser asp leu

FIGURE 7C

NUCLEOTIDE SEQUENCE OF THE LSA GENE
3' END

(CODING 3' END, REPETITIVE)

1 CAAGAACAAACAAAGCGATCTAGAACAAAGAGAGACGT
37 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGATAGACTT
88 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAAGAGAGACTT
139 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATCTAGAACAAAGAGAGACGT
190 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGAGAGACGT
241 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGATAGACTT
292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAAGAGAGACGT
343 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGAGAGACGT
394 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGAGAGACTT
445 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGAGAGACGT
496 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGAGAGACGT
547 GCTAAAGAAAAGTTGCAAGAACAAACAAAGCGATTTAGAACAAAGAGAGACGT
598 GCTAAAGAAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

(CODING 3' END, UNIQUE)

640 AGGAAGGCTGATACGAAAAAAAATTAGAAAGAAAAAGGAACATGGAGAT
691 ATATTAGCAGAGGATTATATGGTCGTTAGAAATACCAGCTATAGAACTT
742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTACCT
793 CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
844 AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
895 CATAAAGGACATCTTGAAGAAAAGATGGTTCAATAAAACCAGAACAA
946 AAAGAAGATAAAATCTGCTGACATACAAAATCATACTAGAGACAGTAAAT
997 ATTTCTGATGTTAATGATTTCAAATAAGTAAGTATGAGGATGAAATAAGT
1048 GCTGAATATGACGATTCTTAATAGATGAAGAAGAAGATGATGAAGACT
1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTCCAAGATGAAGAAA
1150 ACATAGGAATTTATAAAGAACTAGAACAGATTGATAGAGAAAAATGAAAATT
1201 TAGATGATTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG
1252 AAAAATAAAAAAAGGAAAGAAATATGAAAAAACAAGGATAATAATTTA
1303 AACCAAATGATAAAAGTTGTATGATGAGCATATTAAAAATATAAAAATG
1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCAAAATCATTGTTCTA
1405 TATTGACGGAGACAATGAAATTACAGATCGTGGATGAGTTATCTGAAG
1456 ATATAACTAAATATTTATGAAACTATAA (stop)

(NON-CODING 3' END)

1485 AAGGTTATATATT 1498

FIGURE 8

LSA.3'. ALL -> 1-phase Translation

DNA sequence 1496 b.p. CAAAGAACAAACAA ... GGTATATTTT linear

1 / 1	31 / 11
CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA	gln glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln
61 / 21	91 / 31
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT	gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp
121 / 41	151 / 51
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA	leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu glu gln
181 / 61	211 / 71
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT	glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu arg arg
241 / 81	271 / 91
GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT GCT GCT AAA GAA	ala lys glu lys leu gln glu gln gln ser asp leu glu gln asp arg leu ala lys glu
301 / 101	331 / 111
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA	lys leu gln glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln

FIGURE 9A

361 / 121 391 / 131
GAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA
glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln gln
421 / 141 451 / 151
AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA
ser asp leu glu gln glu arg leu ala lys glu lys leu gln glu gln ser asp leu
481 / 161 511 / 171
GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG
glu gln glu arg arg ala lys glu lys leu gln glu gln ser asp leu gln glu gln glu
541 / 181 571 / 191
AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT
arg arg ala lys glu lys leu gln glu gln ser asp leu gln glu gln arg arg ala
601 / 201 631 / 211
AAA GAA AAG TTG CAA GAG CAG CAA AGA GAT TTA GAA CAA AGG AAG GCT GAT ACG AAA AAA
lys glu lys leu gln glu gln arg asp leu gln arg lys ala asp thr lys lys
661 / 221 691 / 231
AAT TTA GAA AGA AAA AAG GAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA
asn leu glu arg lys lys glu his gln asp ile leu ala glu asp leu tyr gln arg leu
721 / 241 751 / 251
GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT CAA
glu ile pro ala ile glu leu pro ser glu asn glu arg gln arg tyr tyr ile pro his gln
781 / 261 811 / 271
TCT TCT CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA
ser ser leu pro gln asp asn arg gln asn ser arg asp ser lys glu ile ser ile ile

FIGURE 9B

FIGURE 9C

1261 / 421 1291 / 431
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT TTT AAA CCA AAT GAT AAA AGT TTG
lys gly lys tyr glu lys thr lys asp asn phe lys pro asn asp lys ser leu
1321 / 441 1351 / 451
TAT GAT GAG CAT ATT AAA TAT AAA TAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asp lys gln val asn lys glu lys glu lys
1381 / 461 1411 / 471
TTC ATT AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp asn glu ile leu gln ile val asp
1441 / 481 1471 / 491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr

FIGURE 9D

LSN. 3' STOP -> 1-phase Translation

DNA sequence 1482 b.p. CAAGAACACAA ... ATGAACTATAA linear

1 / 1 31 / 11
CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA GAA
gln glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln
61 / 21 91 / 31
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT
gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp
121 / 41 151 / 51
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT CTA GAA CAA
leu glu gln glu arg leu ala lys glu gln glu gln gln ser asp leu glu gln
181 / 61 211 / 71
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT
glu arg arg ala lys glu lys leu gln gln ser asp leu glu gln gln glu arg arg
241 / 81 271 / 91
GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA
ala lys glu lys leu gln glu gln gln ser asp leu glu gln asp arg leu ala lys glu
301 / 101 331 / 111
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA
lys leu gln glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln

FIGURE 10A

361 / 121 391 / 131
GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA
glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln gln gln
421 / 141 451 / 151
AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA
ser asp leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu
481 / 161 511 / 171
GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAG
glu gln glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu
541 / 181 571 / 191
AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT
arg arg ala lys glu lys leu gln glu gln gln ser asp leu gln gln gln gln gln gln gln
601 / 201 631 / 211
AAA GAA AAG TTG CAA GAG CAG CAA AGA GAT TTA GAA CAA AGG AAG GCT GAT ACG AAA AAA
lys glu lys leu gln glu gln
661 / 221 691 / 231
AAT TTA GAA AGA AAA AAG GAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA
asn leu glu arg lys lys glu his gly asp ile leu ala glu asp leu tyr gly arg leu
721 / 241 751 / 251
GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT CAA
glu ile pro ala ile glu leu pro ser glu asn glu arg gly tyr tyr ile pro his gln
781 / 261 811 / 271
TCT TCT CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA
ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile ser ile ile

FIGURE 10B

FIGURE 10C

1321 / 441 1351 / 451
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asp lys gln val asn lys glu lys glu lys
1381 / 461 1411 / 471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp
1441 / 481 1471 / 491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu och lys val ile tyr

FIGURE 10D